**In the claims**:

Please amend claims 2-9, 44, 45 and 51-56, and add new claims 57-59 as follows.

2. A method for identifying a compound which modulates interaction or binding between p21 and cyclin D1, the method including:

(a) bringing into contact a first substance which includes a peptide fragment of 40 amino acids or less of p21, or a derivative thereof having at least 70% identity with p21 over a contiguous sequence of at least 5 amino acids, the fragment or derivative comprising an amino acid sequence selected from the group consisting of:

RERWNFDFVTETPLEGDFAW (peptide 4) (SEQ ID NO:4);

KACRRLFGPVDSEQLSRDCD (peptide 2) (SEQ ID NO:2);

**K**xx**RR**y**F**z**P** (wherein x may be any amino acid, y and z may be hydrophobic, and each of the bold residues may be absent or different); (SEQ ID NO:14)

KRRQTSMTDFYHSKRRLIFS (peptide 10) (SEQ ID NO:10);

B1 KRRQTSATDFYHSKRRLIFS (SEQ ID NO:28);

TSMTDFYHSKRRLIFSKRKP (peptide 11) (SEQ ID NO:11);

KRRLIFSK (SEQ ID NO:23); and

xyLzF (wherein y and z are any amino acid and x is preferably R),

with a second substance comprising cyclin D1, or a derivative thereof having at least 70% identity with cyclin D1 over a contiguous sequence of at least 20 amino acids, and a test compound, under conditions wherein, in the absence of the test compound being an inhibitor of interaction or binding of said first and second substances, said first substance and said second substance interact or bind; and

(b) determining interaction or binding between said first substance and said second substance.

3. The method according to claim 2, 44 or 45 wherein the fragment or derivative comprises the amino acid sequence of peptide 4 (SEQ ID NO:4).

4. The method according to claim 2, 44 or 45 wherein the fragment or derivative comprises the amino acid sequence **K**xx**RR**y**F**z**P** (SEQ ID NO:14).

5. The method according to claim 4 wherein the fragment or derivative comprises the amino acid sequence of peptide 2 (SEQ ID NO:2).

6. The method according to claim 2, 44 or 45 wherein the fragment or derivative comprises the amino acid sequence xyLzF.

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7. The method according to claim 6 wherein the fragment or derivative comprises the amino acid sequence of peptide 10 (SEQ ID NO:10).

8. The method according to claim 6 wherein the fragment or derivative comprises the amino acid sequence KRRLIFSK (SEQ ID NO:23).

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9. The method according to claim 8 wherein the fragment or derivative comprises the amino acid sequence of peptide 11 (SEQ ID NO:11).

10. The method according to claim 2, 44 or 45 further comprising testing the ability of the compound to modulate a p21- mediated effect on Cdk4 activity.

44. A method for identifying a compound which modulates interaction or binding between p21 and Cdk4, the method including:

(a) bringing into contact a first substance which includes a peptide fragment of 40 amino acids or less of p21, or a derivative thereof having at least 70% identity with p21 over a contiguous sequence of at least 5 amino acids, the fragment or derivative comprising an amino acid sequence selected from the group consisting of:

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RERWNFDFVTETPLEGDFAW (peptide 4) (SEQ ID NO:4);

KACRRLFGPVDSEQLSRDCD (peptide 2) (SEQ ID NO:2);

**KxxRRyFzP** (wherein x may be any amino acid, y and z may be hydrophobic, and each of the bold residues may be absent or different); (SEQ ID NO:14)

KRRQTSMTDFYHSKRRLIFS (peptide 10) (SEQ ID NO:10);

KRRQTSATDFYHSKRRLIFS (SEQ ID NO:28);

TSMTDFYHSKRRLIFSKRKP (peptide 11) (SEQ ID NO:11);

KRRLIFSK (SEQ ID NO:23); and

xyLzF (wherein y and z are any amino acid and x is preferably R),

with a second substance comprising Cdk4 or a derivative thereof having at least 70% identity with Cdk4 over a contiguous sequence of at least 20 amino acids, and a test compound, under conditions wherein, in the absence of the test compound being an inhibitor of interaction or binding of said first and second substances, said first substance and said second substance interact or bind; and

(b) determining interaction or binding between said first substance and said second substance.

45. A method for identifying a compound which modulates interaction or binding between p21, cyclin D1 and Cdk4, the method including:

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(a) bringing into contact a first substance which includes a peptide fragment of 40 amino acids or less of p21, or a derivative thereof having at least 70% identity with p21 over a contiguous sequence of at least 5 amino acids, the fragment or derivative comprising an amino acid sequence selected from the group consisting of:

RERWNFDFVTETPLEGDFAW (peptide 4) (SEQ ID NO:4);

KACRRLFGPVDSEQLSRDCD (peptide 2) (SEQ ID NO:2);

**K**xx**R**R**y**F**z**P (wherein x may be any amino acid, y and z may be hydrophobic, and each of the bold residues may be absent or different); (SEQ ID NO:14)

KRRQTSMTDFYHSKRRLIFS (peptide 10) (SEQ ID NO:10);

KRRQTSATDFYHSKRRLIFS (SEQ ID NO:28);

TSMTDFYHSKRRLIFSKRKP (peptide 11) (SEQ ID NO:11);

KRRLIFSK (SEQ ID NO:23); and

xyLzF (wherein y and z are any amino acid and x is preferably R),

with a second substance comprising cyclin D1 or a derivative thereof having at least 70% identity with cyclin D1 over a contiguous sequence of at least 20 amino acids, and Cdk4 or a derivative thereof having at least 70% identity with Cdk4 over contiguous sequence of at least 20 amino acids, and a test compound, under conditions wherein, in the absence of the test

compound being an inhibitor of interaction or binding of said first and second substances, said first substance and said second substance interact or bind; and

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(b) determining interaction or binding between said first substance and said second substance.

51. The method of claim 2, 44 or 45 wherein the peptide fragment or derivative is about 40 amino acids or less.

52. The method of claim 2, 44 or 45 wherein the peptide fragment or derivative is about 35 amino acids or less.

53. The method of claim 2, 44 or 45 wherein the peptide fragment or derivative is about 30 amino acids or less.

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54. The method of claim 2, 44 or 45 wherein the peptide fragment or derivative is about 25 amino acids or less.

55. The method of claim 2, 44 or 45 wherein the peptide fragment or derivative is about 20 amino acids or less.

56. The method of claim 2, 44 or 45 wherein the peptide fragment or derivative is about 10 amino acids or less.

57. A method for identifying a compound which modulates interaction or binding between p21 and cyclin D1, the method including:

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(a) bringing into contact a peptide fragment of 40 amino acids or less of p21, or a derivative thereof having at least 70% identity with p21 over a contiguous sequence of at least 5 amino acids, the fragment or derivative comprising an amino acid sequence selected from the group consisting of:

RERWNFDFVTETPLEGDFAW (peptide 4) (SEQ ID NO:4);

KACRRLFGPVDSEQLSRDCD (peptide 2) (SEQ ID NO:2);

KxxRRyFzP (wherein x may be any amino acid, y and z may be hydrophobic, and each of the bold residues may be absent or different); (SEQ ID NO:14)

KRRQTSMTDFYHSKRRLIFS (peptide 10) (SEQ ID NO:10);

KRRQTSATDFYHSKRRLIFS (SEQ ID NO:28);

TSMTDFYHSKRRLIFSKRKP (peptide 11) (SEQ ID NO:11);

KRRLIFSK (SEQ ID NO:23); and

xyLzF (wherein y and z are any amino acid and x is preferably R),

with cyclin D1 and a test compound under conditions wherein in the absence of the test compound said fragment or derivative and cyclin D1 interact or bind; and

(b) determining interaction or binding between said fragment or derivative and cyclin D1 in the presence of said test compound.

58. A method for identifying a compound which modulates interaction or binding between p21 and Cdk4, the method including:

(a) bringing into contact a peptide fragment of 40 amino acids or less of p21, or a derivative thereof having at least 70% identity with p21 over a contiguous sequence of at least 5 amino acids, the fragment or derivative comprising an amino acid sequence selected from the group consisting of:

RERWNFDFVTETPLEGDFAW (peptide 4) (SEQ ID NO:4);

KACRRLFGPVDSEQLSRDCD (peptide 2) (SEQ ID NO:2);

KxxRRyFzP (wherein x may be any amino acid, y and z may be hydrophobic, and each of the bold residues may be absent or different); (SEQ ID NO:14)

KRRQTSMTDFYHSKRRLIFS (peptide 10) (SEQ ID NO:10);

KRRQTSATDFYHSKRRLIFS (SEQ ID NO:28);

TSMTDFYHSKRRLIFSKRKP (peptide 11) (SEQ ID NO:11);

KRRLIFSK (SEQ ID NO:23); and

xyLzF (wherein y and z are any amino acid and x is preferably R),

with Cdk4 and a test compound under conditions wherein in the absence of the test compound said fragment or derivative and Cdk4 interact or bind; and

(b) determining interaction or binding between said fragment or derivative and Cdk4 in the presence of said test compound.

59. A method for identifying a compound which modulates interaction or binding between p21, cyclin D1 and Cdk4, the method including:

(a) bringing into contact a peptide fragment of 40 amino acids or less of p21, or a derivative thereof having at least 70% identity with p21 over a contiguous sequence of at least 5 amino acids, the fragment or derivative comprising an amino acid sequence selected from the group consisting of:

RERWNFDFVTETPLEGDFAW (peptide 4) (SEQ ID NO:4);

KACRRLFGPVDSEQLSRDCD (peptide 2) (SEQ ID NO:2);

KxxRRyFz**P** (wherein x may be any amino acid, y and z may be hydrophobic, and each of the bold residues may be absent or different); (SEQ ID NO:14)

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KRRQTSMTDFYHSKRRLIFS (peptide 10) (SEQ ID NO:10);

KRRQTSATDFYHSKRRLIFS (SEQ ID NO:28);

TSMTDFYHSKRRLIFSKRKP (peptide 11) (SEQ ID NO:11);

KRRLIFSK (SEQ ID NO:23); and

xyL$_2$F (wherein y and z are any amino acid and x is preferably R),

with a cyclin D1, Cdk4 and a test compound under conditions wherein in the absence of the test compound said fragment or derivative, cyclin D1 and Cdk4 interact or bind; and

(b) determining interaction or binding between said fragment or derivative, cyclin D1 and Cdk4 in the presence of the test compound.